

SUPPLEMENTARY MATERIAL

Figure S1. Phylogenetic analysis of SDH/TDH genes in bacteria (black text) and animals (blue text). Bootstrap values are indicated for nodes with $\geq 50\%$ support.

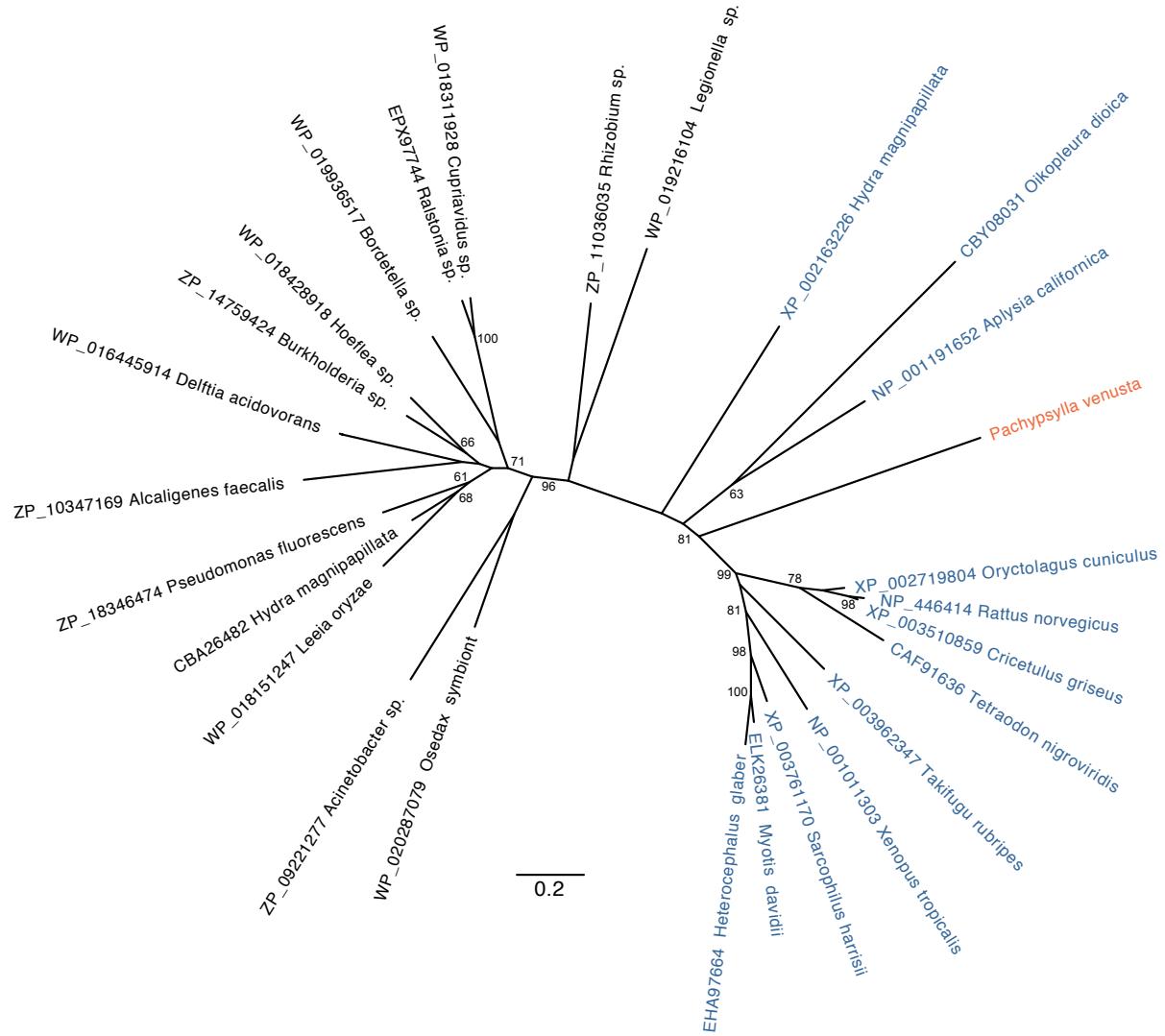


Figure S2. Sense and antisense expression of the psyllid BCAT gene in the bacteriome and the rest of the body. Note the 10-fold difference in scale between the sense and antisense plots. The references used for mapping was the BCAT coding sequence. The pronounced dip in antisense coverage reflects the presence of an intron between positions 345 and 346 in the coding sequence. The positions of introns are noted with black triangles at the base of the sense plot/

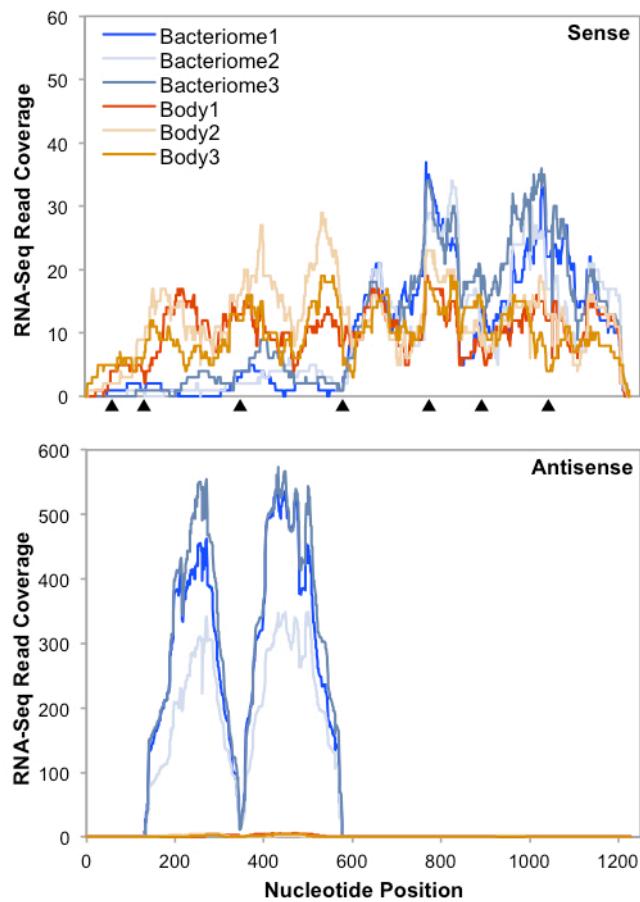
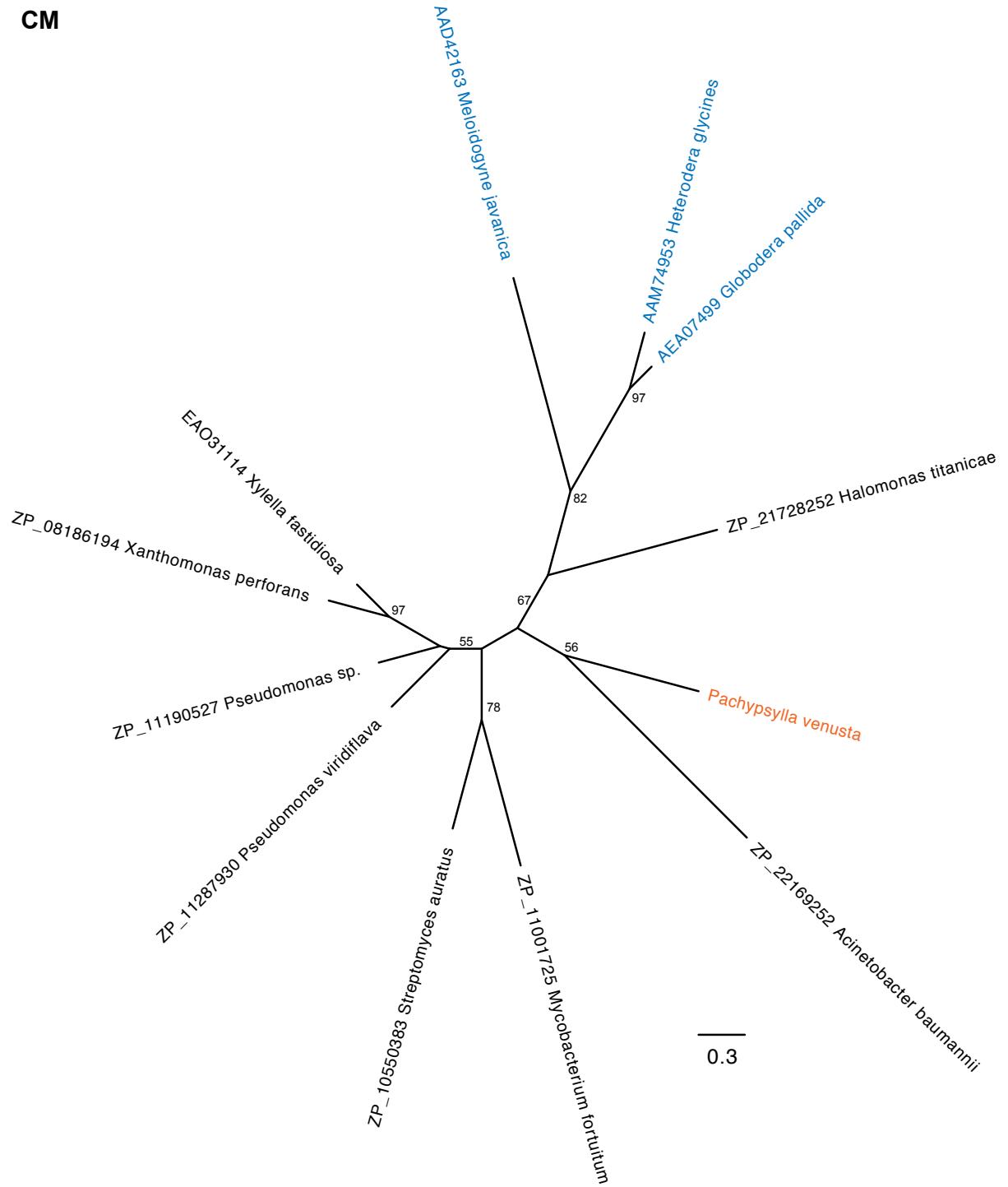
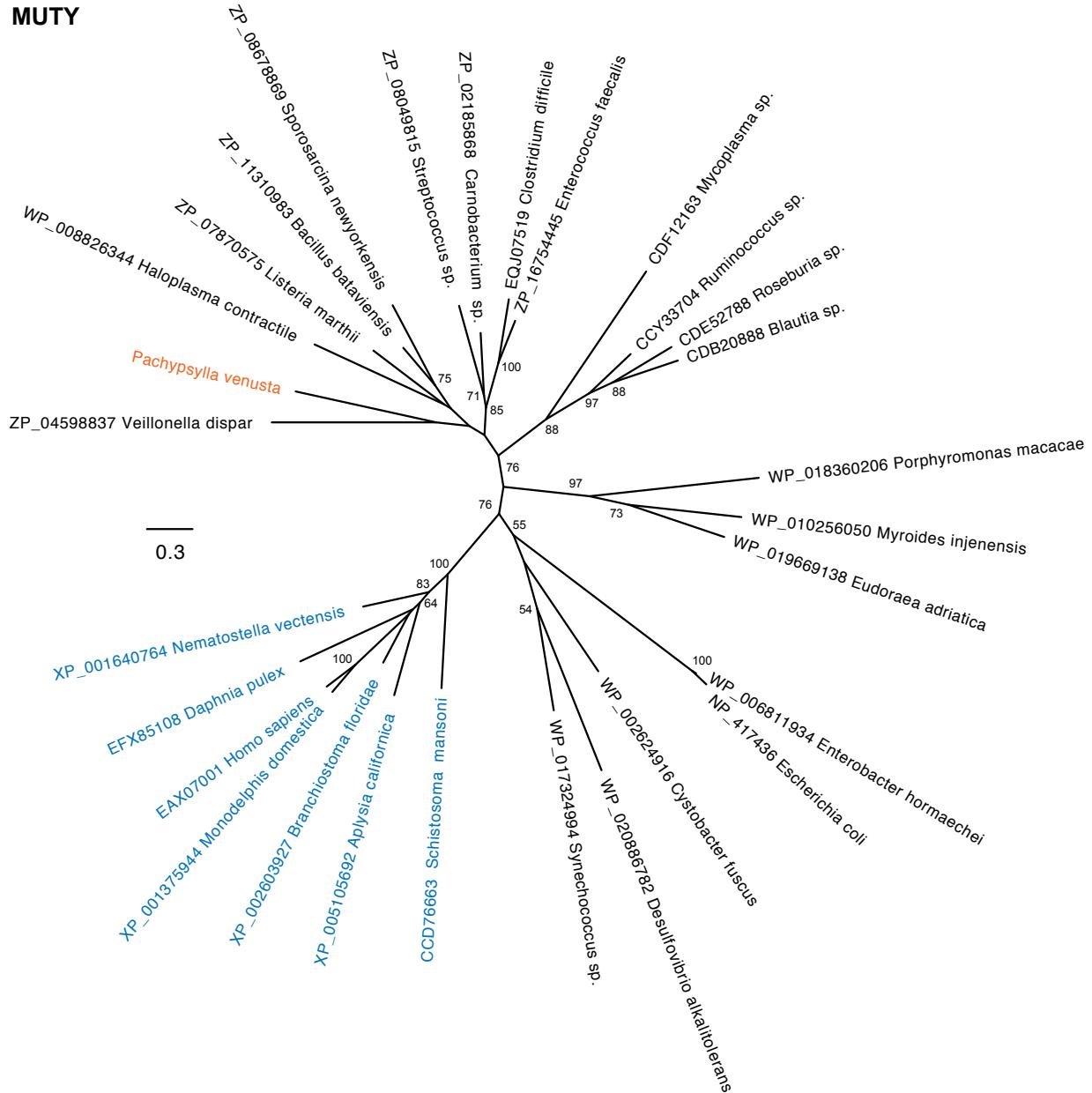


Figure S3. Phylogenetic analyses of *Pachypsylla venusta* genes that appear to have been acquired from bacteria (see Table 3). Bootstrap values are indicated for nodes with $\geq 50\%$ support. Sequences from other animal lineages are highlighted in blue (for genes for which alignable animal sequences were obtained). Phylogenetic analysis was not performed on the highly divergent and diverse ankyrin repeat-containing and AAA-ATPase gene families.

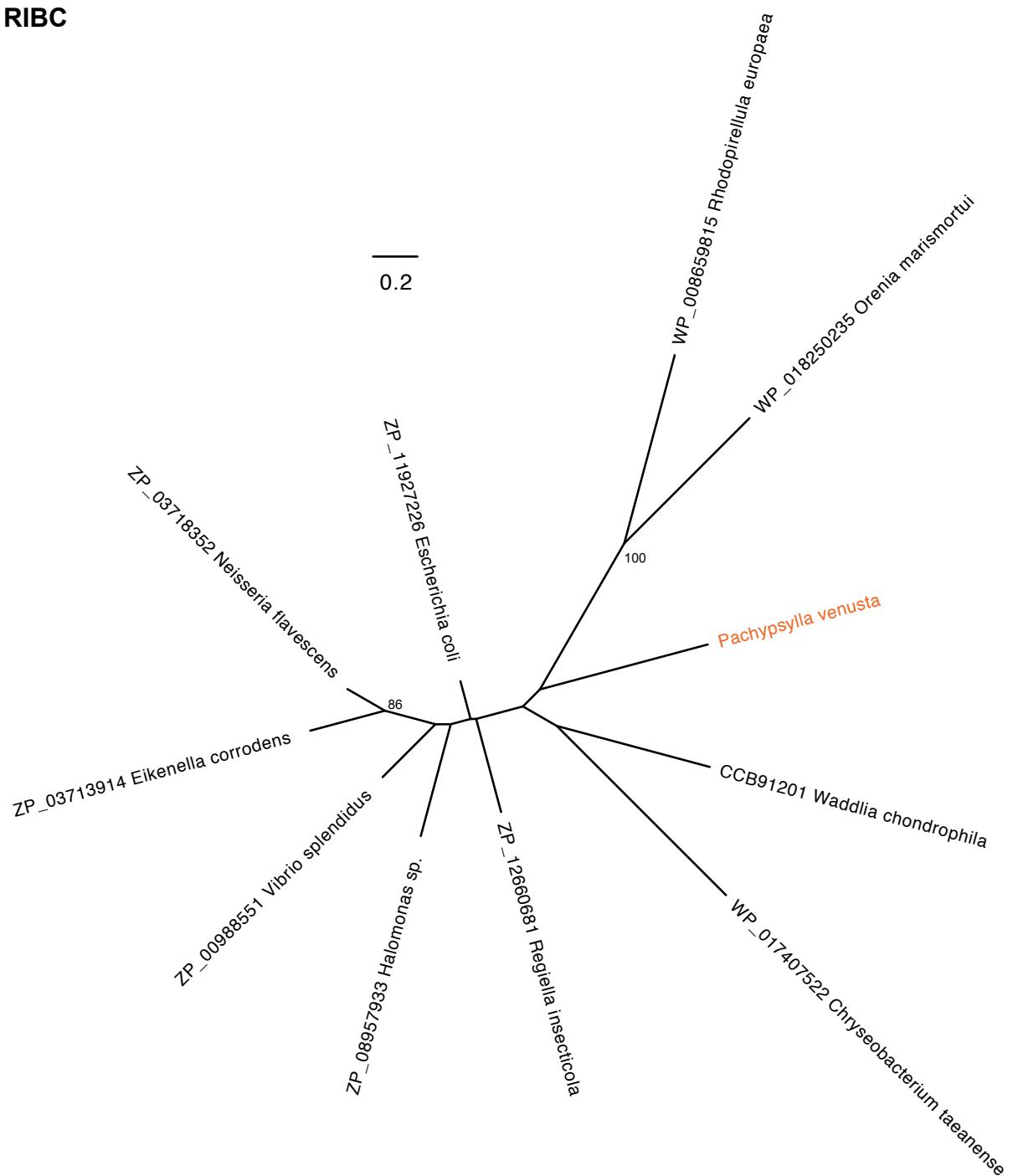
CM

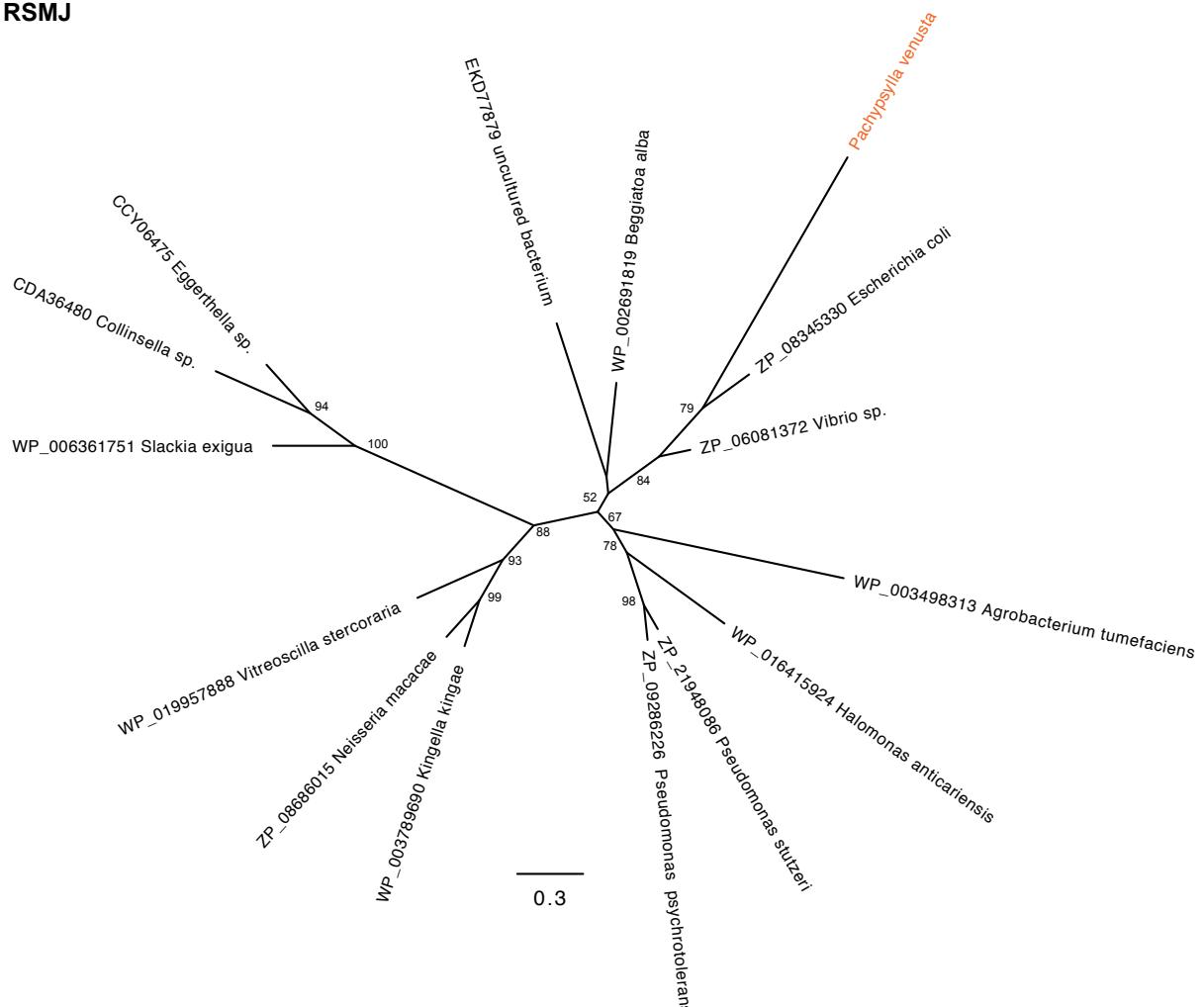


MUTY



RIBC





YDCJ

